

#3



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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Serial No.: 09/981,206
Filed: October 17, 2001
Confirmation No.: 5790
Applicant(s): Samuel I. Achilefu et al.
For (title): **CARBOCYANINE DYES FOR TANDEM, PHOTODIAGNOSTIC
AND THERAPEUTIC APPLICATIONS**
Atty Docket: MRD-74

Cincinnati, Ohio 45202

December 26, 2001

Box SEQUENCE
Assistant Commissioner for Patents
Washington, D.C. 20231

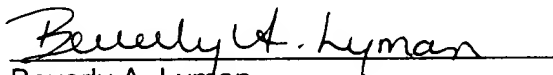
Sir:

STATEMENT UNDER 37 C.F.R. §1.821(f)

The information recorded in computer readable form of United States Patent Application, Express Mail No. EL576790364US, filed October 17, 2001, and the paper copy of same are identical to the written sequence listing contained in the above-referenced application and contain no new matter.

Respectfully submitted,

WOOD, HERRON & EVANS, L.L.P.


Beverly A. Lyman
Reg. No. 41,961

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RAW SEQUENCE LISTING ERROR REPORT

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/981,206

Source: OIPE

Date Processed by STIC: 11/2/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/981,206

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☒ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

Does Not Comply
Corrected Diskette Needed
Errors on pp. 1-3

3 <110> APPLICANT: Achilefu, Samuel I.
4 Rajagopalan, Raghavan
5 Dorshow, Richard B.
6 Bugaj, Joseph E.
8 Mallinckrodt Inc.
10 <120> TITLE OF INVENTION: Carbocyanine Dyes For Tandem, Photodiagnostic
11 and Therapeutic Applications
13 <130> FILE REFERENCE: MRD-74
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/981,206
16 <141> CURRENT FILING DATE: 2001-10-17
W--> 18 <150> PRIOR APPLICATION NUMBER:
W--> 19 <151> PRIOR FILING DATE: Do not respond if no other prior application include
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: PatentIn Version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 8
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
W--> 31 <221> NAME/KEY: MOD RES → put underscore between MOD + RES → MOD_RES
32 <222> LOCATION: (1)...(8)
33 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe. Artificial sequence is completely synthesized.
34
35 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an
36 intramolecular disulfide bond between two Cys
37 amino acids. Artificial sequence is completely synthesized.
38 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp. Artificial sequence is completely synthesized.
39
41 <400> SEQUENCE: 1
W--> 42 Xaa Xaa Tyr Xaa Lys Thr Xaa Thr
43 1 5
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 8
49 <212> TYPE: PRT
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
W--> 53 <221> NAME/KEY: MOD RES
54 <222> LOCATION: (1)...(8)
55 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe. Artificial sequence is completely synthesized.
56
57 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an
58 intramolecular disulfide bond between two Cys
59 amino acids. Artificial sequence is completely synthesized.
61 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp. Artificial sequence is completely synthesized.
62
63 <223> OTHER INFORMATION: Xaa at location 8 represents Thr-OH. Artificial sequence is completely synthesized.
64

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

66 <400> SEQUENCE: 2
W--> 67 Xaa Xaa Tyr Xaa Lys Thr Xaa Xaa
68 1 5
71 <210> SEQ ID NO: 3
72 <211> LENGTH: 11
73 <212> TYPE: PRT
74 <213> ORGANISM: Peptide *Unknown A/Bombesin*
76 <400> SEQUENCE: 3 - invalid; see error summary sheet, item 10
77 Gly Ser Gly Gln Trp Ala Val Gly His Leu Met
78 1 5 10
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 11
83 <212> TYPE: PRT
84 <213> ORGANISM: Peptide -- same
86 <400> SEQUENCE: 4
87 Gly Asp Gly Gln Trp Ala Val Gly His Leu Met
88 1 5 10
92 <210> SEQ ID NO: 5
93 <211> LENGTH: 8
94 <212> TYPE: PRT
95 <213> ORGANISM: Peptide - Same
97 <400> SEQUENCE: 5
98 Asp Tyr Met Gly Trp Met Asp Phe
99 1 5
102 <210> SEQ ID NO: 6
103 <211> LENGTH: 8
104 <212> TYPE: PRT
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
W--> 108 <221> NAME/KEY: MOD RES
109 <222> LOCATION: (1)...(8)
110 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine. Artificial
111 sequence is completely synthesized.
113 <400> SEQUENCE: 6
W--> 114 Asp Tyr Xaa Gly Trp Xaa Asp Phe
115 1 5
118 <210> SEQ ID NO: 7
119 <211> LENGTH: 8
120 <212> TYPE: PRT
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
W--> 124 <221> NAME/KEY: MOD RES
125 <222> LOCATION: (1)...(8)
126 <223> OTHER INFORMATION: Xaa at location 1 represents D-Asp. Artificial sequence is
127 completely synthesized.
128 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine. Artificial
129 sequence is completely synthesized.
131 <400> SEQUENCE: 7
W--> 132 Xaa Tyr Xaa Gly Trp Xaa Asp Phe

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

```

133      1              5
137 <210> SEQ ID NO: 8
138 <211> LENGTH: 8
139 <212> TYPE: PRT
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
W--> 143 <221> NAME/KEY: MOD RES
144 <222> LOCATION: (1)...(8)
145 <223> OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
146      completely synthesized.
148 <400> SEQUENCE: 8
W--> 149 Xaa Pro Arg Arg Pro Tyr Ile Leu
150      1              5

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:25

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

L:15 M:270 C: Current Application Number differs, Replaced Application Number
 L:18 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
 L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
 L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
 L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
 L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:124 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 L:143 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
 L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8